



1600

RAW SEQUENCE LISTING

DATE: 03/19/2003

PATENT APPLICATION: US/09/446,634A

TIME: 12:59:24

Input Set : A:\09-446,634 Sequence Listing.txt

Output Set: N:\CRF4\03192003\I446634A.raw

THE

3 <110> APPLICANT: Ono Pharmaceutical Co., Ltd.

5 <120> TITLE OF INVENTION: NOVEL PLASMID DNA COMPRISING REPORTER GENE DNA AND USE OF

6 SAME

8 <130> FILE REFERENCE: Q57282

10 <140> CURRENT APPLICATION NUMBER: 09/446,634A

11 <141> CURRENT FILING DATE: 1999-12-23

13 <150> PRIOR APPLICATION NUMBER: JP 9-171440

14 <151> PRIOR FILING DATE: 1997-06-27

16 <160> NUMBER OF SEQ ID NOS: 23

18 <170> SOFTWARE: PatentIn version 3.2

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 37

22 <212> TYPE: DNA

23 <213> ORGANISM: Artificial Sequence

25 <220> FEATURE:

26 <223> OTHER INFORMATION: Primer F1

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33 <211> LENGTH: 32

34 <212> TYPE: DNA

35 <213> ORGANISM: Artificial Sequence

37 <220> FEATURE:

38 <223> OTHER INFORMATION: Primer R1

40 <400> SEQUENCE: 2

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44 <210> SEQ ID NO: 3

45 <211> LENGTH: 26

46 <212> TYPE: DNA

47 <213> ORGANISM: Artificial Sequence

49 <220> FEATURE:

50 <223> OTHER INFORMATION: Primer F2

52 <400> SEQUENCE: 3

53 aaccagcacc atctggtcgc gatggt 26

56 <210> SEQ ID NO: 4

57 <211> LENGTH: 26

58 <212> TYPE: DNA

59 <213> ORGANISM: Artificial Sequence

61 <220> FEATURE:

62 <223> OTHER INFORMATION: Primer R2

64 <400> SEQUENCE: 4

65 aggtgtggct gatctgaagg aactca 26

68 <210> SEQ ID NO: 5

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69 <211> LENGTH: 26
70 <212> TYPE: DNA
71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: Primer F3
76 <400> SEQUENCE: 5
77 agaaatgacc atgggtgaca cagaga 26
80 <210> SEQ ID NO: 6
81 <211> LENGTH: 26
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: Primer R3
88 <400> SEQUENCE: 6
89 aaatgttggc agtggctcag gactct 26
92 <210> SEQ ID NO: 7
93 <211> LENGTH: 26
94 <212> TYPE: DNA
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Primer F4
100 <400> SEQUENCE: 7
101 agatcagcca tggagcagcc acagga 26
104 <210> SEQ ID NO: 8
105 <211> LENGTH: 26
106 <212> TYPE: DNA
107 <213> ORGANISM: Artificial Sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: Primer R4
112 <400> SEQUENCE: 8
113 attggagtct gcagggaggc ctgggt 26
116 <210> SEQ ID NO: 9
117 <211> LENGTH: 37
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: Primer F5
124 <400> SEQUENCE: 9
125 gcaagcttca ccatgaagct actgtcttct atcgaac 37
128 <210> SEQ ID NO: 10
129 <211> LENGTH: 33
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Primer R5
136 <400> SEQUENCE: 10
137 agccatggcc ggcgatacag tcaactgtct ttg 33
140 <210> SEQ ID NO: 11
141 <211> LENGTH: 62

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142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: Primer F6
148 <400> SEQUENCE: 11
149 gccatggctc ctaagaagaa gcgtaaggta ggatcccata atgccatcag gtttgggcgg      60
151 at                                                                    62
154 <210> SEQ ID NO: 12
155 <211> LENGTH: 69
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Primer R6
162 <400> SEQUENCE: 12
163 cctctagact agctggcata gtcgggcacg tcgtaggggt agtcgacgta caagtccttg      60
165 tagatctcc                                                            69
168 <210> SEQ ID NO: 13
169 <211> LENGTH: 33
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Primer F7
176 <400> SEQUENCE: 13
177 cacggatccc acaacgcgat tcgttttgga cga                                33
180 <210> SEQ ID NO: 14
181 <211> LENGTH: 33
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Primer R7
188 <400> SEQUENCE: 14
189 atggtcgacg tacatgtccc tgtagatctc ctg                                33
192 <210> SEQ ID NO: 15
193 <211> LENGTH: 33
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Primer F8
200 <400> SEQUENCE: 15
201 cacggatccc acaacgctat ccgttttggt cgg                                33
204 <210> SEQ ID NO: 16
205 <211> LENGTH: 33
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Primer R8
212 <400> SEQUENCE: 16
213 atggtcgacg tacatgtcct tgtagatctc ctg                                33
216 <210> SEQ ID NO: 17

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217 <211> LENGTH: 38
218 <212> TYPE: DNA
219 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Multiple cloning site DNA linker - sense strand
224 <400> SEQUENCE: 17
225 gaattcgctcg acggtaccga tatcgagctc gcggccgc 38
228 <210> SEQ ID NO: 18
229 <211> LENGTH: 85
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Gal4 responsive element
236 <400> SEQUENCE: 18
237 tcgacggagt actgtcctcc gcgacggagt actgtcctcc gcgacggagt actgtcctcc 60
239 gcgacggagt actgtcctcc gagct 85
242 <210> SEQ ID NO: 19
243 <211> LENGTH: 20
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Gal4 responsive element
250 <400> SEQUENCE: 19
251 cgacggagta ctgtcctccg 20
254 <210> SEQ ID NO: 20
255 <211> LENGTH: 9
256 <212> TYPE: PRT
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Influenza hemagglutinin epitope
262 <400> SEQUENCE: 20
264 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
265 1 5
268 <210> SEQ ID NO: 21
269 <211> LENGTH: 38
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Multiple cloning site DNA linker - antisense strand
276 <400> SEQUENCE: 21
277 gcggccgcga gctcgatc ggtaccgtcg acgaattc 38
280 <210> SEQ ID NO: 22
281 <211> LENGTH: 335
282 <212> TYPE: PRT
283 <213> ORGANISM: Homo sapiens
286 <220> FEATURE:
287 <221> NAME/KEY: mat_peptide
288 <222> LOCATION: (17)..(355)
290 <400> SEQUENCE: 22

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292 Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
293      -15                -10                -5                -1
296 Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
297 1          5          10          15
300 Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
301      20          25          30
304 Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
305      35          40          45
308 Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
309      50          55          60
312 Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
313 65          70          75          80
316 Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
317      85          90          95
320 Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
321      100         105         110
324 Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
325      115         120         125
328 Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
329      130         135         140
332 Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
333 145         150         155         160
336 Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
337      165         170         175
340 Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
341      180         185         190
344 Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu
345      195         200         205
348 Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met
349      210         215         220
352 Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu
353 225         230         235         240
356 Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu
357      245         250         255
360 Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys
361      260         265         270
364 Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys
365      275         280         285
368 Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser
369      290         295         300
372 Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
373 305         310         315
376 <210> SEQ ID NO: 23
377 <211> LENGTH: 327
378 <212> TYPE: PRT
379 <213> ORGANISM: Mus musculus
382 <220> FEATURE:
383 <221> NAME/KEY: mat_peptide
384 <222> LOCATION: (22)..(327)

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VERIFICATION SUMMARY

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